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Genotyping of MC4R gene (G923>T) and its association with productive performance and carcass traits in Ross 308

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ABSTRACT

This study was aimed to select MC4R gene as a candidate gene for growth and carcass traits in Ross 308. The productive characteristics were studied weekly for 42 days for 100 chicks numbered individually. Blood samples were collected from chickens at 21 days old, Genotypes of MC4R were obtained using PCR products sequence. In this study, DNA sequencing data for the MC4R gene was detected technique SNP(G923>T) (1050bp) with three genotype appeared as (GG- GT- TT). However, the results show that a highly significant differences (P<0.01) between the MC4R genotype and body weight, weight gain, leg length and drumstick weight, with a significantly differences (P<0.05) in all of breast depth, drumstick length, carcass weight, back weight, weight of wings and abdominal fat weight. There was no variation detected in body length, breast circumference, drumstick circumference, breast, Neck, Liver, Heart and Gizzard weight. The MC4R gene SNP (G923>T) could be considered as a candidate marker gene for the early chicken selection program for growth and some carcass traits. The abstract must be no longer than 250 words and must clearly emphasise the objective of the study.

Key words: broiler chickens, growth traits, melanocortin-4 gene, SNP.

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INTRODUCTION

Selection strategies for broilers focused on quantitative traits that aimed to enhance growth rates and meat productivity, due to the necessity of meeting the growing nutritional needs of the world population. With this expected increase in the population and with advancing age, the world will need more food at a rate of (70-100%) by the year 2050 AD, as the world population is expected to reach 9 billion people (Khumpeerawat et al.,2021); (Chau et al., 2022), By conducting research on mutations in useful genes (candidate genes) and their relationship to economic traits to determine the genetic basis for production traits and to develop single nucleotide polymorphism SNP molecular genetics tests (nucleic acid tests) as a method of selection in breeding and genetic improvement projects (Thu et al., 2021); (Aboelhassan et al., 2023), A number of studies have demonstrated the relationship between polymorphisms of candidate genes (specifically SNPs or genotypes) (Hekmat and Abdulkareem, 2026), and a range of chicken production traits that include growth and body composition (Wang et al., 2009); (Fathi et al., 2018), Such as, a few studies have been conducted using (SNPs) based genotyping of candidate genes to enhance the genetic potential of chickens of broiler production purposes, Many polymorphisms have been correlated with broiler body weight (BW), growth hormone (GH) (Fontanesi et al., 2012), pituitary specific transcription factor-1(pit 1) gene (Nie et al., 2008), Perilipin 1 (PLIN1 Gene) (Abdulkareem et al., 2025), Insulin-like growth factor 1 (IGF-1 gene) (Hosnedlova et al., 2020). It has been found that the central melanocortin (MC4R) system plays an essential role in the control of nutrition and body weight. Previous studies have indicated the importance of melanocortins and their receptors have become a target for physiological processes in several pathways. Including energy balance, reproduction, cardiovascular functions, body growth, regulation of tissue development, and many other functions in mammals and birds (Yi et al., 2018); (Thunet al., 2021), Melanocortins are polypeptides consisting of a group of small protein hormones and are derived from the

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precursor of proopiomelanocortin (POMC) (Dores and Lecaude, 2005), which produces adrenocorticotropic hormone (ACTH) and is a major producer of melanocortin in cells. Corticosteroids in the anterior pituitary gland (Cawley et al., 2016). It plays an important role in regulating energy balance in birds, as in mammals, and is involved in regulating feed intake as well as metabolism and body weight (Li and Li, 2006); (Radwan, 2023), Few researches have been published to acquaintance the effect of MC4R mutations on growth production traits in broiler chickens. this study related to the effects of MC4R gene polymorphisms and SNP on production traits and carcass traits in broiler chickens Ross 308.

MATERIALS AND METHODS

This study was conducted at Poultry field of College of Agricultural engineering sciences /University of Baghdad, for the period from 27/9/2023 to 8/11/2023, to detecting polymorphism of (MC4R) gene and its related with growth characteristics, determine their genotypes, their allelic frequency, and the percentage of genotypes in the group of experimental units, and to study the relationship of these combinations with some economic traits and carcass traits in broiler chickens Ross 308. The study includes 100/chick of hybrid Ross 308 one day old with a mean initial body weight of 44.91 g/birds. Numbered Individually and raced in a deep litter in a closed system, the experimental diets was formulated for isocaloric and insoitrogenic according to the guide of (Dale, 1994), they were fed by starter diet which Contains 21.5% crude protein and 2988 (Kcal/Kg), and grower diets contains of 19.5% crude protein and 3100 (Kcal/Kg), while finisher diets contains of 18% crude protein and 3160 (Kcal/Kg), Initial and weekly measurements were taken all of Body Weight, Body Length, Breast Circumference, Breast Depth, Leg Length, Drumstick Length, Drumstick Circumference. At the last week /42 day old, the chickens were slaughtered and the carcasses were cuts to breast, Drumstick, back, neck, wings, heart, liver, Gizzard and abdominal fat, their relative weight was calculated according to (Aviagen catalogue. 2022) Blood samples were collected from 100 chicken at 21rd day from the wing vein in EDTA-coated tubes, DNA extraction started by using extraction kit (Biolabs nebs monarch kits), and to assess the purity of the samples DNA and concentration measurement using Standard procedure for nucleic acid quantification by Qubit 4 and it was about 17-25 (ng/µL) The primers were prepared to work according to the instructions of the supplying company (Macrogen Humanizing Genomics).

F: TCAGAGGAATGCAAAAAGGAC
R: GCTGTATGCTGAATACACAGTA

band size(1050 bp)- gene region (chromosome 2, exon 1).

Detection or Sequencing: 25 µl of PCR amplification reaction contained 12.5 µl from One Taq (NEB ®) mastermix, 3 µl of DNA sample, 1.5µl 10 pmol/µl from each primer and 6.5 µl of free-nuclease water, The 35 amplification cycles utilized included 1 min of denaturation at (94°C), 3 min of extension at (72°C), and one last 5 min of extension at 72°C. UV trans-illumination on a 1.5 % agarose gel revealed the PCR results, and it was prepared by adding (10 of TBI, 90 of water. Then 4 µl of Red Safe dye was added to the gel and the mixture was left to cool (50°C). After pouring the gel into the transfer dishes, the samples are loaded by adding 5 µl of the PCR product in wells, except for the first well in which only 4 microliters of DNA Ladder is placed, after which the lid is placed and an electric current of 80 volts/1hr. More than 20µl PCR product from each sample were send to macrogen /Korea for sequencing by Sanger method to identify the single nucleotide polymorphism. Analysis of sequence FASTA files have been done by Geneious Prime software and aligned to RefSeq of MC4R gene. Statistical analysis of the data was carried out using the statistical analysis system SAS (SAS, 2012) program, to study the influence of the treatment on the different characterization and according to the significant comparative between the means in the Duncan (Duncan,1955) polynomial test. The genotype frequency distribution was tested for Hardy Weinberg equilibrium using a chi squared ($\chi 2$) test. Association analyses between genotypes of MC4R.

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RESULTS AND DISCUSSION

To explain the results for the process of extracting DNA for MC4R gene by using electrophoresis after amplifying the required fragment with using (PCR) technique for samples it produce one loci with band size 1050 bp. (Figure 1).

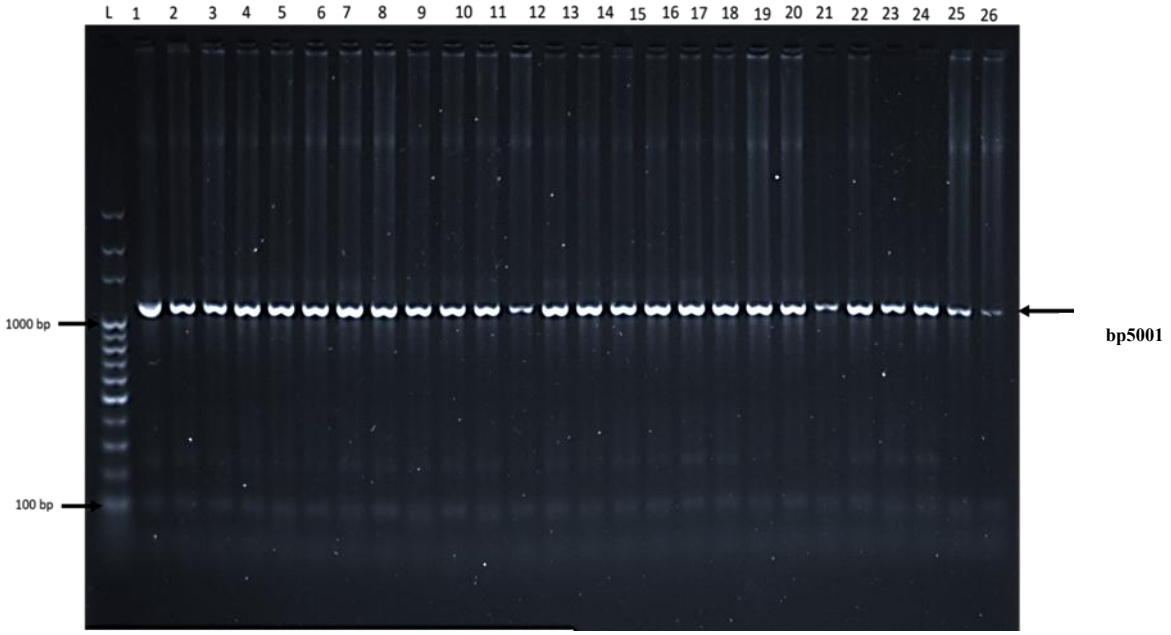

Figure 1. Electrophoresis of PCR product for MC4R gene (size 1050bp), ladder of DNA (1500)bp.

To shows the polymorphisms and genotypes of MC4R gene Arranging the nucleotide sequence of DNA samples by using the Sequence program (for analyzing the DNA sequence). variations. The SNP at position (923) showed three genetic combinations appeared (Figure 2). And were classified based on homozygous and hetero gene. Which represents the wild type GG, followed by individuals carrying the hybrid genotype GT, then individuals carrying the mutant TT genotype, which represents the mutant type.

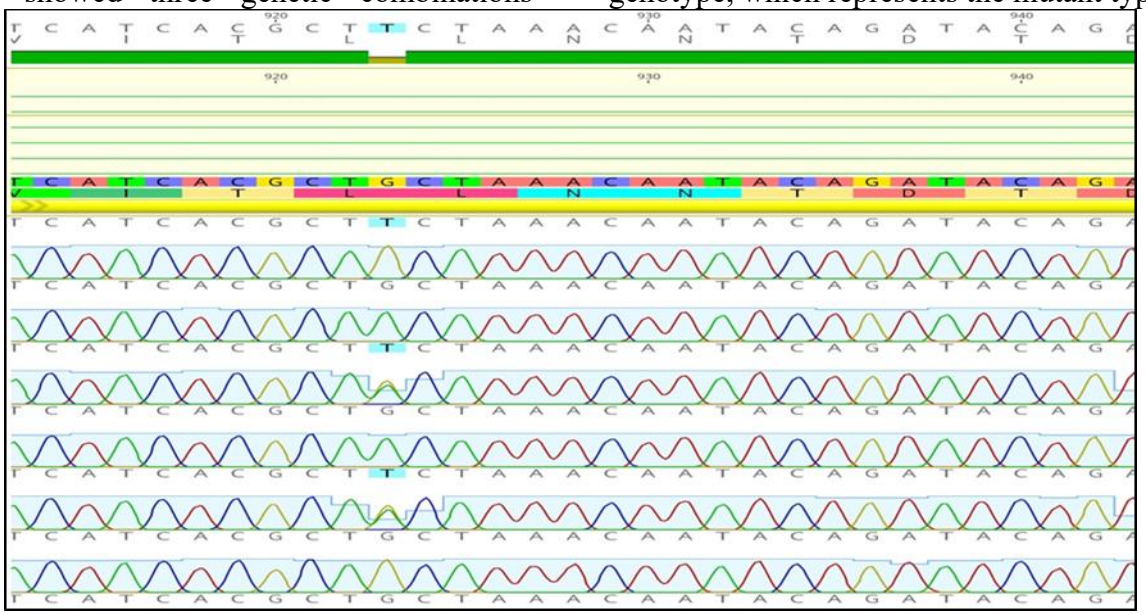

Figure 2. Shows single nucleotide polymorphisms SNP (G923>T) of the MC4R gene

(Table 1) shows the genotypes and allele frequencies for MC4R gene in Ross 308, was high frequency ($p<0.01$) between distribution of genotypes GG ,GT and TT with 17.07%, 39.36% and 43.62% respectively, also there were highly significant ($p<0.01$) in allele frequencies for G and T allel with frequency 0.37, 0.63 respectively.

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Table1. Number and percentage of MC4R gene of Ross 308

Genotype	No. of hens	Genotypic percentage	Allele	Allele Frequency
GG	16	17.02	G	0.37
GT	37	39.36	T	0.63
TT	41	43.62	-	**
Total	94	% 100	-	
χ^2		17.553**		
P-value	(P<0.01)			

(Table 2) shows the effect of the genotypes GG, GT, and TT for SNP in MC4R gene on body weight trait, it shown that there are highly significant differences (p<0.01) between the GG and GT genotypes at 3rd week with 1011.29 gm. and 916.09 gm. respectively, also with 4th week with 1411.93 gm. and 1309.11 gm. for GG and GT respectively, at 5th week GG and TT were superior than GT with means 2229.17gm., 2111.36 gm. and 1841.25 gm., while at 6th week showed superiority for GG genotype with 3119.60 gm. but no significant differences between the genotypes on 0, 1 and 2 weeks. This result is consistent with what (Aboelhassan et al., 2023) pointed out in his study on the relationship of this gene with growth characteristics, body weight, Drumstick, and breast, as well as it is consistent with other studies that indicated a relationship between body weight and mutations occurring in this gene, this relationship between the genetic makeup of MC4R gene and body weight, also deal with (Xuemei et al., 2006) and with (Aggag and El-Sabrout, 2018) studies, they found that MC4R gene plays a role in controlling feed behavior, and thus affects the body weight, It also agree with (Fathi et al., 2018) who analyze the correlation between genetic variation of MC4R gene and productive performance in turkeys, and they found a highly significant effect (P<0.01) between genotypes and live body weight.

Table 2. Relationship of genetic polymorphism of the MC4R gene SNP (G923>T) on the average initial and weekly body weight in Ross 308

Genotypes	Body weight/ gm.						
	0 wk	1 wk	2 wk	3 wk	4 wk	5 wk	6 wk
GG	45.20± 1.32	192.73± 4.50	482.40± 12.94	1011.29± 29.71a	1411.93± 45.02a	2229.17± 100.32a	3119.60± 147.77 a
GT	43.55± 0.73	193.27± 3.59	467.44± 7.61	916.09± 20.43 b	1309.11± 22.33b	1841.25± b53.05 b	2578.52± 61.62b
TT	44.21± 0.63	196.41± 4.38	467.51± 9.11	963.92± 19.10ab	1381.61± 24.71ab	2111.36± 83.29a	2831.74± 61.01b
p-value	N.S	N.S	N.S	**	**	**	**

Values with different letters contents indicate significant differences. ** indicates the presence of significant differences between the genotypes at a significant level (P<0.01).

To study the effect of SNP for MC4R gene on body weight gain, it seem there are no significant differences between the genotypes for this traits at 1st, 2nd, 4th, 5th and 6th week, with exception for 3rd week which was with highly significant differences (p<0.01) for GG and GT genotype with means 512.14 gm. and 448.95 gm. respectively, also for total weight gain seam was with highly significant differences (p<0.01) for GG with 3076.80 gm. compared with 2535.56 gm. and 2787.61 gm. for GT and TT genotype respectively, **(Table 3).** indicates a relationship between SNP in this gene and the trait of body weight gain, (Bo, 2022); (Sharma et al., 2008) suggested that some polymorphisms of the MC4R gene may be associated with increased body weight and feed conversion efficiency in chickens, and the reason for the presence of variation in this trait between weeks is that the genes responsible for weight and weight gain may change with age in broilers (Sharma et al., 2008), and they operate in on-off system, causing many changes in the animal's body.

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Table 3. Relationship of genetic polymorphism of the MC4R gene SNP(G923>T) on the average weekly and total body weight gain in broilers Ross 308

Genotypes	Body weight gain/ gm.						
	1 wk	2 wk	3 wk	4 wk	5 wk	6 wk	Total
GG	147.53± 4.68	289.66 ± 10.56	512.14± 24.281a	413.28± 53.29	45.8 730.00±9	868.33± 151.66	3076.80± 146.59a
GT	149.72± 3.23	274.16± 5.28	448.95 ± 12.48 b	411.68± 16.71	554.56± 49.94	879.08± 54.32	2535.56± 61.43 b
TT	152.19± 4.05	271.09 ± 7.21	479.88 ± 9.69 ab	442.64± 18.26	607.50 ± 61.90	878.77± 60.213	2787.61± 60.47b
p-value	N.S	N.S	**	N.S	N.S	N.S	**

Values with different letters contents indicate significant differences. ** indicates the presence of significant differences between the genotypes at a significant level (P<0.01).

To explain the effect of the genetic manifestations of MC4R gene genotype on the average primary and weekly for body length trait, it seems there is no significant differences between genotypes GG, GT, and TT during the different weeks along the experiment. (Table 4.)

Table 4. Relationship of genetic polymorphism of the MC4R gene SNP (G923>T) on the initial and weekly body length in broilers Ross 308

Genotypes	body length/ cm						
	0 wk	1 wk	2 wk	3 wk	4 wk	5 wk	6 wk
GG	22.26± 0.22	27.60 ± 0.40	34.07 ± 0.35	42.00± 0.83	±46.46 0.47	53.70 ± 0.53	57.16± 1.97
GT	22.08± 0.16	±27.115 0.24	34.48± 0.19	41.64± 0.52	46.02± 0.26	52.83± 0.46	57.50± 0.70
TT	22.07± 0.16	±27.58 0.27	33.96± 0.26	42.25± 0.37	45.560± 0.32	52.90 ± 0.34	78.62± 19.72
p-value	N.S	N.S	N.S	N.S	N.S	N.S	N.S

N.S not significant.

Also to study the effect of MC4R gene SNPs on breast circumference (Table 5). shows that there were no significant effect between the genotypes GG, GT, and TT for MC4R gene on breast circumference during the different weeks of the experiment.

Table 5. Relationship of genetic polymorphism of the MC4R gene SNP (G923>T) on the initial and weekly breast circumference in broilers Ross 308

Genotypes	breast circumference/ cm						
	0 wk	1 wk	2 wk	3 wk	4 wk	5 wk	6 wk
GG	± 210.3 0.27	14.00± 0.70	18.50± 0.17	24.40± 0.50	28.10 ± 0.39	34.75± 0.35	41.00± 1.22
GT	10.33 ± 0.13	13.14± 0.29	18.21± 0.16	23.65 ± 0.59	27.72 ± 0.24	33.63± 0.38	39.87± 0.39
TT	10.28± 0.10	13.30± 0.23	18.35± 0.17	24.66± 0.28	28.09± 0.22	34.00± 0.38	40.45± 0.52
p-value	N.S	N.S	N.S	N.S	N.S	N.S	N.S

N.S not significant.

And for the breast depth (Table 6). explain that there were no significant differences in the average initial and weekly, with the exception of the 6th week, as it was found that there were highly significant differences (p<0.01) in the GG than GT genotype. It is clear from results that GG genotype was superior at 6th week, and this result was consistent with tables 5 , as the superiority of this formula in breast depth is complementary to its superiority in body weight and weight gain.

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Table 6. Relationship of genetic polymorphism of the MC4R gene SNP (G923>T) on the initial and weekly breast depth in broilers Ross 308

Genotypes	breast depth/ cm						
	0 wk	1 wk	2 wk	3 wk	4 wk	5 wk	6 wk
GG	3.21± 0.10	6.70± 0.20	8.13± 0.17	10.83± 0.10	11.40± 0.19	17.30± 0.58	18.50± 0.28a
GT	3.52± 0.10	6.28± 0.12	8.43± 0.11	10.79 ± 0.18	11.45± 0.12	16.67± 0.41	17.08± 0.17b
TT	3.36± 0.09	6.45± 0.19	8.42± 0.11	10.93 ± 0.13	11.68± 0.12	17.52± 0.42	17.73 ± 0.33 ab
p-value	N.S	N.S	N.S	N.S	N.S	N.S	*

Values with different letters contents indicate significant differences. * indicates the presence of significant differences between the genotypes at a significant level (P<0.05).

About the effect of the relationship between genotypes of gene with the characteristic of primary and weekly leg length, there are no significant differences between the genotypes GG, GT, and TT for primary length and for all experimental weeks except the third and sixth weeks, as highly significant differences ($p<0.01$) were found. (Table 7). The GG genotype over the GT genotype and there were no significant differences between GG and GT genotype and TT genotype in the 3rd week with means of 24.60 cm., 24.27 cm. and 23.64 cm., and the GG genotype was differ with highly significant to the GT and TT genotype with mean 36.25 cm. for GG genotype in the 6th week. This consistent with the study of (Wang et al., 2009), which showed the relationship of SNP in MC3R and MC4R genes and indicated that there is a relationship between these mutations and body weight, leg length, and carcass weight.

Table 7. The relationship of genetic polymorphism of the MC4R gene SNP (G923>T) on the initial and weekly leg length in broilers Ross 308

Genotypes	Leg length/ cm						
	0 wk	1 wk	2 wk	3 wk	4 wk	5 wk	6 wk
GG	12.03 ± 0.15	13.75± 0.47	19.92 ± 0.22	24.60 ± 0.40 a	27.33 ± 0.318	29.30 ± 0.583	36.25± a2.096
GT	± 211.9 0.19	13.03± 0.27	19.64 ± 0.21	23.64 ± 0.19 b	26.86 ± 0.178	28.125 ± 0.326	33.69± b0.336
TT	11.68 ± 0.15	13.36± 0.29	19.56± 0.22	24.27± 0.22 ab	26.87 ± 0.210	±29.00 0.555	±34.16 0.406 b
p-value	N.S	N.S	N.S	**	N.S	N.S	**

Values with different letters contents indicate significant differences. ** indicates the presence of significant differences between the genotypes at a significant level (P<0.01).

(Table 8). indicate no significant differences in the average primary and weekly Drumstick length between the genotypes GG, GT, and TT, except for the sixth week, but there were significant differences ($p<0.05$) between the genotypes for GG with 21.25 cm while was 19.16 cm., 19.30 cm. for GT and TT respectively. The results of the sixth week indicate that there is an association between the polymorphism of MC4R gene with Drumstick length. This is consistent with the study of (Li and Li, 2006) and with (Xuemei et al., 2006).

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Table8. The relationship of genetic polymorphism of the MC4R gene SNP(G923>T) on the initial and weekly drumstick length in broilers Ross 308

Genotypes	Drumstick length / cm						
	0 wk	1 wk	2 wk	3 wk	4 wk	5 wk	6 wk
GG	±6.13	7.64 ±	±10.42	13.10±	±15.40	±15.42	±21.25
	0.379	0.496	0.250	0.458	0.289	0.297	1.314a
GT	5.93±	±7.08	10.24 ±	12.23±	15.13±	±15.20	±19.16
	0.195	0.243	0.198	0.172	0.191	0.274	0.333b
TT	5.90 ±	±6.94	10.35±	12.68±	15.73±	±16.00	19.30 ±
	0.174	0.238	0.216	0.214	0.181	0.389	0.409b
p-value	N.S	N.S	N.S	N.S	N.S	N.S	*

Values with different letters contents indicate significant differences. * indicates the presence of significant differences between the genotypes at a significant level (P<0.05).

For the effect of genotypes GG, GT, and TT for SNP in the MC4R gene on Drumstick circumference (Table 9). shows that there were no significant differences between genotypes in the average initial and weekly Drumstick circumference.

Table 9. Relationship of genetic polymorphism of the MC4R gene SNP (G923>T) on the initial and weekly drumstick circumference in broilers Ross 308

Genotypes	Drumstick circumference / cm						
	0 wk	1 wk	wk2	3 wk	4 wk	5 wk	6 wk
GG	4.23±	5.33±	8.07±	9.80±	11.60± ±	\14.42	16.75±
	0.127	0.333	0.164	0.583	0.362	0.611	1.030
GT	4.15±	5.03±	8.01±	9.68±	11.43±	13.68±	16.54±
	0.071	0.140	0.099	0.133	0.141	0.223	0.248
TT	4.24±	5.35±	8.17±	9.90±	11.31±	14.31±	16.82±
	0.089	0.186	0.135	0.159	0.147	0.161	0.205
p-value	N.S	N.S	N.S	N.S	N.S	N.S	N.S

N.S not significant.

For the carcass traits (Table 10). shows there was significant differences (p<0.05) for GG genotype with 2330.50 gm. compared with 1973.27 and 2137.61 gm. for GT and TT. respectively for carcass weight, and was highly significant (p<0.01) for drumstick weight for GG genotype compared with GT and TT, and for back weight was also significant for GG genotype with 384.50 gm. compared with GT genotype, same for weight of wings was also significant for GG genotype with 218.25 gm. compared with GT 190.95 gm. also abdominal fat weight showed significant differeces between GG genotype compared with GT and TT genotype with means 36.25, 32.40 and 32.00gm. respectively, while there was no significant differences between the genotypes in the average weight of the breast, neck, liver, heart, and gizzard. The reason for the presence of significant differences between the genotypes in some carcass characteristics may be due to the role of the gene and the significant effect of the polymorphism of this gene on the final body weight, weight gain, body dimensions, and its reflection on the weight of the flocks later. This indicates the fundamental role of this gene, which controls the process of eating food, and appetite and its effect on the animal's weight through the deposition of fat in the body and the formation of muscles, and this was confirmed by (Al-jburi, A and R. Senkal. 2023) when they studied goats. When studying the relationship between this gene and body weight and carcass characteristics, they found that (Sharma et al., 2008) suggested that some polymorphisms of the MC4R gene may be associated with increased body weight or feed conversion efficiency in chickens, and (Musa, 2006) indicated that there is a significant positive relationship between Live weight, carcass weight, breast muscle weight, leg muscle weight, heart weight, liver weight, and abdominal fat weight.

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Table 10. The relationship of the genetic manifestations of the MC4R gene SNP(G923>T) to the Caracas traits, and the abdominal fat in broilers Ross 308

Traits (gm.)	Genotypes			P-Value
	GG	GT	TT	
Carcass weight	a81.752 ± 2330.50	± b46.100 1973.27	ab53.744± 2137.61	*
Breast weight	52.504± 952.75	21.934± 817.54	43.124± 883.56	N.S
Drumstick weight	a20.227± 648.00	b14.303± 525.22	± b14.174 573.34	**
Back weight	a11.507± 384.50	b7.786 ± 325.95	ab9.969 ± 358.30	*
Neck weight	3.3416 ± 135.00	3.352± 121.09	± 3.042 131.65	N.S
Weight of wings	± a2.428 218.25	b4.505± 190.95	ab6.380 ± 208.73	*
Liver weight	3.719 ± 52.00	2.016± 50.90	2.216± 55.65	N.S
Heart weight	0.645 ± 15.50	0.558± 12.72	0.626± 14.69	N.S
Gizzard weight	1.931± 37.75	0.878 ± 36.13	1.170 ± 38.478	N.S
Abdominal fat weight	a ± 4.007 36.25	b ± 1.871 32.40	b ± 1.411 32.00	*

Values with different letters contents indicate significant differences. ** indicates the presence of significant differences between the genotypes at a significant level (P<0.01). * indicates the presence of significant differences between the genotypes at a significant level (P<0.05).

CONCLUSION

A relationship exists between polymorphisms of the MC4R gene and some of the studied productive traits in Ross 308 broiler chickens, The results showed a significant difference between the genotypes in SNP 1, with the wild-type GG being superior in most traits, including body weight, weight gain, breast depth, leg length, and drumstick length, as well as in some carcass traits, and abdominal fat. This assists in selecting individuals with superior growth and productive performance in Ross 308 broiler chickens. Identifying desirable genotypes at an early age and understanding their genetic structures and the desirable traits they possess can be used in selection programs.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest regarding the publication of this manuscript.

AUTHORS DECLARATION

We confirm that all Figures and Tables in the manuscript are original, entirely created by the authors as part of our own work, and no images or tables from other sources or individuals have been utilized.

AUTHOR CONTRIBUTIONS

M. Ameen was responsible for experimental design, research execution, and manuscript drafting. [Al-Anbari] provided academic supervision, methodological guidance, and critical review of the manuscript. All authors have read and approved the final version for publication.

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الطرز الوراثية لجين MC4R (G923>T) وعلاقتها مع الاداء الانتاجي و صفات الذبيحة في روز 308

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المستخلص

هدفت هذه الدراسة إلى انتخاب جين MC4R كجين مرشح لصفات النمو والذبيحة في روز 308. تمت دراسة الصفات الإنتاجية أسبوعيا لمدة 42 يوما لعدد 100 فرخ مرقم بشكل فردي. تم جمع عينات الدم من الدجاج بعمر 21 يوما، وتم الحصول على التراكيب الوراثية لجين MC4R باستخدام تسلسل منتج PCR. في هذه الدراسة تم الكشف عن بيانات تسلسل الحمض النووي لجين MC4R بتقنية SNP (1050bp) (G923>T) مع ظهور ثلاثة تراكيب وراثية هي (GG- GT- TT). عموماً، أظهرت النتائج وجود فروق ذات دلالة إحصائية عالية (P<0.01) بين التركيب الوراثية لجين MC4R و وزن الجسم، الزيادة الوزنية، طول الرجل، وزن الفخذ، مع وجود اختلافات معنوية (P<0.05) في كل من عمق الصدر، طول الفخذ، وزن الذبيحة، وزن الظهر، وزن الأجنحة و وزن دهون البطن. لم يتم الكشف عن اي اختلاف معنوي في طول الجسم، محيط الصدر، محيط الفخذ، وزن الصدر، الرقبة والكبد والقلب والقانصة. يمكن اعتبار الجين SNP MC4R (G923>T) جينًا محددًا مرشحًا لبرنامج انتخاب الدجاج المبكر لصفات النمو و بعض صفات الذبيحة.

الكلمات المفتاحية: دجاج اللاحم، صفات النمو، جين ميلانوكورتين 4، SNP.